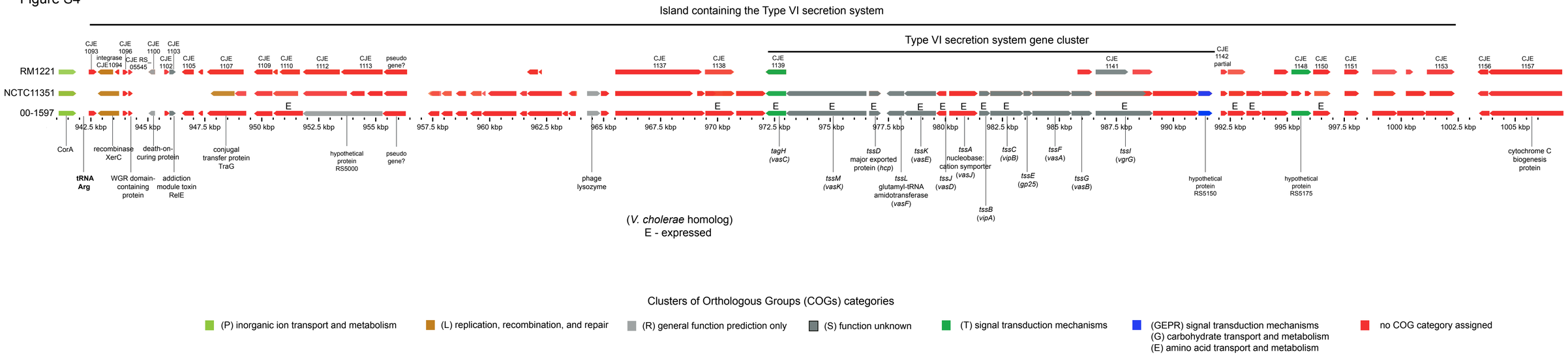
Figure S4


Island containing the Type VI secretion system
Type VI secretion system gene cluster
RM1221
NCTC11351
00-1597
CJE 1093
integrase CJE1094
CJE 1096
CJE RS_ 05545
CJE 1100
CJE 1103
CJE 1102
CJE 1105
CJE 1107
CJE 1109
CJE 1110
CJE 1112
CJE 1113
pseudo gene?
CJE 1137
CJE 1138
CJE 1139
CJE 1141
CJE 1142 partial
CJE 1148
CJE 1150
CJE 1151
CJE 1153
CJE 1156
CJE 1157
942.5 kbp
945 kbp
947.5 kbp
950 kbp
952.5 kbp
955 kbp
957.5 kbp
960 kbp
962.5 kbp
965 kbp
967.5 kbp
970 kbp
972.5 kbp
975 kbp
977.5 kbp
980 kbp
982.5 kbp
985 kbp
987.5 kbp
990 kbp
992.5 kbp
995 kbp
997.5 kbp
1000 kbp
1002.5 kbp
1005 kbp
CorA
tRNA Arg
recombinase XerC
WGR domain-containing protein
death-on-curing protein
addiction module toxin RelE
conjugal transfer protein TraG
hypothetical protein RS5000
pseudo gene?
phage lysozyme
tagH (vasC)
tssM (vasK)
tssD major exported protein (hcp)
tssL glutamyl-tRNA amidotransferase (vasF)
tssK (vasE)
tssA nucleobase: cation symporter (vasJ)
tssJ (vasD)
tssB (vipA)
tssC (vipB)
tssE (gp25)
tssF (vasA)
tssG (vasB)
tssI (vgrG)
hypothetical protein RS5150
hypothetical protein RS5175
cytochrome C biogenesis protein
E
(V. cholerae homolog)
E - expressed
Clusters of Orthologous Groups (COGs) categories
(P) inorganic ion transport and metabolism
(L) replication, recombination, and repair
(R) general function prediction only
(S) function unknown
(T) signal transduction mechanisms
(GEPR) signal transduction mechanisms
(G) carbohydrate transport and metabolism
(E) amino acid transport and metabolism
no COG category assigned